

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/377,316DATE: 10/13/95
TIME: 16:40:43

INPUT SET: S6614.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Murgita, Robert A.
6
7 (ii) TITLE OF INVENTION: RECOMBINANT HUMAN ALPHA-FETOPROTEIN AS A
8 CELL PROLIFERATIVE AGENT
9
10 (iii) NUMBER OF SEQUENCES: 16
11
12 (iv) CORRESPONDENCE ADDRESS:
13 (A) ADDRESSEE: Fish & Richardson P.C.
14 (B) STREET: 225 Franklin Street, Suite 3100
15 (C) CITY: Boston
16 (D) STATE: MA
17 (E) COUNTRY: USA
18 (F) ZIP: 02110-2804
19
20 (v) COMPUTER READABLE FORM:
21 (A) MEDIUM TYPE: Floppy disk
22 (B) COMPUTER: IBM PC compatible
23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
25
26 (vi) CURRENT APPLICATION DATA:
27 (A) APPLICATION NUMBER: US 08/377,316
28 (B) FILING DATE: 24-JAN-1995
29 (C) CLASSIFICATION:
30
31 (viii) ATTORNEY/AGENT INFORMATION:
32 (A) NAME: Clark, Paul T.
33 (B) REGISTRATION NUMBER: 30,162
34 (C) REFERENCE/DOCKET NUMBER: 06727/006001
35
36 (ix) TELECOMMUNICATION INFORMATION:
37 (A) TELEPHONE: (617) 542-5070
38 (B) TELEFAX: (617) 542-8906
39 (C) TELEX: 200154
40
41
42 (2) INFORMATION FOR SEQ ID NO:1:
43
44 (i) SEQUENCE CHARACTERISTICS:
45 (A) LENGTH: 2022 base pairs
46 (B) TYPE: nucleic acid

ENTERED

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47 (C) STRANDEDNESS: single
48 (D) TOPOLOGY: linear
49
50 (ii) MOLECULE TYPE: DNA
51
52
53
54
55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
56
57 ATATTGTGCT TCCACCACTG CCAATAACAA AATAACTAGC AACCATGAAG TGGGTGGAAT 60
58
59 CAATTTTTTTT AATTTTCCTA CTAAATTTTA CTGAATCCAG AACACTGCAT AGAAATGAAT 120
60
61 ATGGAATAGC TTCCATATTG GATTCTTACC AATGTACTGC AGAGATAAGT TTAGCTGACC 180
62
63 TGGCTACCAT ATTTTTTGGC CAGTTTGTTC AAGAAGCCAC TTACAAGGAA GTAAGCAAAA 240
64
65 TGGTGAAAGA TGCATTGACT GCAATTGAGA AACCCACTGG AGATGAACAG TCTTCAGGGT 300
66
67 GTTTAGAAAA CCAGCTACCT GCCTTTCTGG AAGAACTTTG CCATGAGAAA GAAATTTTGG 360
68
69 AGAAGTACGG ACATTCAGAC TGCTGCAGCC AAAGTGAAGA GGAAGACAT AACTGTTTTTC 420
70
71 TTGCACACAA AAAGCCCACT GCAGCATGGA TCCCACTTTT CCAAGTTCCA GAACCTGTCA 480
72
73 CAAGCTGTGA AGCATATGAA GAAGACAGGG AGACATTCAT GAACAAATTC ATTTATGAGA 540
74
75 TAGCAAGAAG GCATCCCTTC CTGTATGCAC CTACAATTCT TCTTTCGGCT GCTGGGTATG 600
76
77 AGAAAAATAAT TCCATCTTGC TGCAAAGCTG AAAATGCAGT TGAATGCTTC CAAACAAAGG 660
78
79 CAGCAACAGT TACAAAAGAA TTAAGAGAAA GCAGCTTGTT AAATCAACAT GCATGTCCAG 720
80
81 TAATGAAAAA TTTTGGGACC CGAACTTTCC AAGCCATAAC TGTTACTAAA CTGAGTCAGA 780
82
83 AGTTTACCAA AGTTAATTTT ACTGAAATCC AGAACTAGT CCTGGATGTG GCCCATGTAC 840
84
85 ATGAGCACTG TTGCAGAGCA GATGTGCTGG ATTGTCTGCA GGATGGGGAA AAAATCATGT 900
86
87 CCTACATATG TTCTCAACAA GACACTCTGT CAAACAAAAT AACAGAATGC TGCAAACCTGA 960
88
89 CCACGCTGGA ACGTGGTCAA TGTATAATTC ATGCAGAAAA TGATGAAAAA CCTGAAGGTC 1020
90
91 TATCTCCAAA TCTAAACAGG TTTTTAGGAG ATAGAGATTT TAACCAATTT TCTTCAGGGG 1080
92
93 AAAAAAATAT CTTCTTGGCA AGTTTTGTTC ATGAATATTC AAGAAGACAT CCTCAGCTTG 1140
94
95 CTGTCTCAGT AATTCTAAGA GTTGCTAAAG GATACCAGGA GTTATTGGAG AAGTGTTTCC 1200
96
97 AGACTGAAAA CCCTCTTGAA TGCCAAGATA AAGGAGAAGA AGAATTACAG AAATACATCC 1260
98
99 AGGAGAGCCA AGCATTGGCA AAGCGAAGCT GCGGCCTCTT CCAGAACTA GGAGAATATT 1320

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100
101 ACTTACAAAA TGAGTTTCTC GTTGCTTACA CAAAGAAAGC CCCCAGCTG ACCTCGTCGG 1380
102
103 AGCTGATGGC CATCACCAGA AAAATGGCAG CCACAGCAGC CACTTGTTGC CAACTCAGTG 1440
104
105 AGGACAAACT ATTGGCCTGT GGCAGGGGAG CGGCTGACAT TATTATCGGA CACTTATGTA 1500
106
107 TCAGACATGA AATGACTCCA GTAAACCCTG GTGTTGGCCA GTGCTGCACT TCTTCATATG 1560
108
109 CCAACAGGAG GCCATGCTTC AGCAGCTTGG TGGTGGATGA AACATATGTC CCTCCTGCAT 1620
110
111 TCTCTGATGA CAAGTTCATT TTCCATAAGG ATCTGTGCCA AGCTCAGGGT GTAGCGCTGC 1680
112
113 AAAGGATGAA GCAAGAGTTT CTCATTAACC TTGTGAAGCA AAAGCCACAA ATAACAGAGG 1740
114
115 AACAACTTGA GGCTCTCATT GCAGATTTCT CAGGCCTGTT GGAGAAATGC TGCCAAGGCC 1800
116
117 AGGAACAGGA AGTCTGCTTT GCTGAAGAGG GACAAAAACT GATTTCAAAA ACTGGTGCTG 1860
118
119 CTTTGGGAGT TTAAATTACT TCAGGGGAAG AGAAGACAAA ACGAGTCTTT CATTCCGGTGT 1920
120
121 GAACTTTTCT CTTTAATTTT AACTGATTTA ACACTTTTGT TGAATTAATG ATAAAGACTT 1980
122
123 TTATGTGAGA TTTCCCTTATC ACAGAAATAA AATATCTCCA AA 2022
124

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 590 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: Not Relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Thr Leu His Arg Asn Glu Tyr Gly Ile Ala Ser Ile Leu Asp Ser Tyr
1 5 10 15
Gln Cys Thr Ala Glu Ile Ser Leu Ala Asp Leu Ala Thr Ile Phe Phe
20 25 30
Ala Gln Phe Val Gln Glu Ala Thr Tyr Lys Glu Val Ser Lys Met Val
35 40 45
Lys Asp Ala Leu Thr Ala Ile Glu Lys Pro Thr Gly Asp Glu Gln Ser
50 55 60
Ser Gly Cys Leu Glu Asn Gln Leu Pro Ala Phe Leu Glu Glu Leu Cys

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	65	70	75	80
153				
154				
155	His Glu Lys Glu Ile Leu Glu Lys Tyr Gly His Ser Asp Cys Cys Ser			
156		85	90	95
157				
158	Gln Ser Glu Glu Gly Arg His Asn Cys Phe Leu Ala His Lys Lys Pro			
159		100	105	110
160				
161	Thr Ala Ala Trp Ile Pro Leu Phe Gln Val Pro Glu Pro Val Thr Ser			
162		115	120	125
163				
164	Cys Glu Ala Tyr Glu Glu Asp Arg Glu Thr Phe Met Asn Lys Phe Ile			
165		130	135	140
166				
167	Tyr Glu Ile Ala Arg Arg His Pro Phe Leu Tyr Ala Pro Thr Ile Leu			
168		145	150	155
169				
170	Leu Ser Ala Ala Gly Tyr Glu Lys Ile Ile Pro Ser Cys Cys Lys Ala			
171		165	170	175
172				
173	Glu Asn Ala Val Glu Cys Phe Gln Thr Lys Ala Ala Thr Val Thr Lys			
174		180	185	190
175				
176	Glu Leu Arg Glu Ser Ser Leu Leu Asn Gln His Ala Cys Pro Val Met			
177		195	200	205
178				
179	Lys Asn Phe Gly Thr Arg Thr Phe Gln Ala Ile Thr Val Thr Lys Leu			
180		210	215	220
181				
182	Ser Gln Lys Phe Thr Lys Val Asn Phe Thr Glu Ile Gln Lys Leu Val			
183		225	230	235
184				240
185	Leu Asp Val Ala His Val His Glu His Cys Cys Arg Ala Asp Val Leu			
186		245	250	255
187				
188	Asp Cys Leu Gln Asp Gly Glu Lys Ile Met Ser Tyr Ile Cys Ser Gln			
189		260	265	270
190				
191	Gln Asp Thr Leu Ser Asn Lys Ile Thr Glu Cys Cys Lys Leu Thr Thr			
192		275	280	285
193				
194	Leu Glu Arg Gly Gln Cys Ile Ile His Ala Glu Asn Asp Glu Lys Pro			
195		290	295	300
196				
197	Glu Gly Leu Ser Pro Asn Leu Asn Arg Phe Leu Gly Asp Arg Asp Phe			
198		305	310	315
199				320
200	Asn Gln Phe Ser Ser Gly Glu Lys Asn Ile Phe Leu Ala Ser Phe Val			
201		325	330	335
202				
203	His Glu Tyr Ser Arg Arg His Pro Gln Leu Ala Val Ser Val Ile Leu			
204		340	345	350
205				

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206 Arg Val Ala Lys Gly Tyr Gln Glu Leu Leu Glu Lys Cys Phe Gln Thr
207           355                      360                      365
208
209 Glu Asn Pro Leu Glu Cys Gln Asp Lys Gly Glu Glu Glu Leu Gln Lys
210           370                      375                      380
211
212 Tyr Ile Gln Glu Ser Gln Ala Leu Ala Lys Arg Ser Cys Gly Leu Phe
213           385                      390                      395                      400
214
215 Gln Lys Leu Gly Glu Tyr Tyr Leu Gln Asn Glu Phe Leu Val Ala Tyr
216           405                      410                      415
217
218 Thr Lys Lys Ala Pro Gln Leu Thr Ser Ser Glu Leu Met Ala Ile Thr
219           420                      425                      430
220
221 Arg Lys Met Ala Ala Thr Ala Ala Thr Cys Cys Gln Leu Ser Glu Asp
222           435                      440                      445
223
224 Lys Leu Leu Ala Cys Gly Glu Gly Ala Ala Asp Ile Ile Ile Gly His
225           450                      455                      460
226
227 Leu Cys Ile Arg His Glu Met Thr Pro Val Asn Pro Gly Val Gly Gln
228           465                      470                      475                      480
229
230 Cys Cys Thr Ser Ser Tyr Ala Asn Arg Arg Pro Cys Phe Ser Ser Leu
231           485                      490                      495
232
233 Val Val Asp Glu Thr Tyr Val Pro Pro Ala Phe Ser Asp Asp Lys Phe
234           500                      505                      510
235
236 Ile Phe His Lys Asp Leu Cys Gln Ala Gln Gly Val Ala Leu Gln Arg
237           515                      520                      525
238
239 Met Lys Gln Glu Phe Leu Ile Asn Leu Val Lys Gln Lys Pro Gln Ile
240           530                      535                      540
241
242 Thr Glu Glu Gln Leu Glu Ala Leu Ile Ala Asp Phe Ser Gly Leu Leu
243           545                      550                      555                      560
244
245 Glu Lys Cys Cys Gln Gly Gln Glu Gln Glu Val Cys Phe Ala Glu Glu
246           565                      570                      575
247
248 Gly Gln Lys Leu Ile Ser Lys Thr Gly Ala Ala Leu Gly Val
249           580                      585                      590
250

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Not Relevant
- (D) TOPOLOGY: linear